

GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test ($P(X \geq k)$), Benjamini-Hochberg FDR-corrected across all tested pairs. Corroborated Shared Genes: count of shared genes backed by ≥ 2 distinct disease_gdp.main_source values combined across both diseases (e.g. GWAS-backed for one, ClinVar-backed for the other still counts); Shared Gene Names lists each gene's own source count in parentheses. Overlap Coefficient: shared genes / MIN(each disease's own total gene count) -- complements the Jaccard-based Similarity Score by showing how much of the SMALLER disease's entire known gene-set is covered by this pair, which Jaccard (dividing by the union) can understate. Shared Cluster: cluster id if both diseases fall in the same label-propagation cluster (scripts/build_disease_clusters.php), blank otherwise. See scripts/build_related.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-11 03:00:14. Filters applied: disease name contains "Native american myopathy" (4 matching pairs). · Rows: 4 · Generated: 2026-10-11 18:17:37

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Liver neoplasms	Native american myopathy	1	1	STAC3 (3)	0.00654	1.00000	9.871e-3	1.120e-2	
Hepatomegaly	Native american myopathy	1	1	STAC3 (3)	0.01695	1.00000	3.767e-3	4.809e-3	
Congenital myopathy	Native american myopathy	1	1	STAC3 (4)	0.02174	1.00000	2.922e-3	3.876e-3	
Bailey-Bloch congenital myopathy	Native american myopathy	1	1	STAC3 (4)	0.50000	1.00000	6.494e-5	2.331e-4	